The paragraph beginning at line 42 on page 20 of the application as filed, has been replaced with paragraph revised as follows:

--In general, the largest rescued plasmid is used to design new primers to sequence the full-length genomic insertion. Such primers may be designed using a computer program, for example, the Primer3 program found on the Internet using the website from the Whitehead Institute for Biomedical Research/MIT.--

B3

The paragraph beginning at line 6 on page 25 of the application as filed, has been replaced with paragraph revised as follows:

The sequencing resulted in identification of a 4437 bp DNA sequence (Figures 9A-9B, SEQ ID NO:26). A Basic BLASTN search of non-redundant nucleic acid sequence databases, conducted on Feb. 29, 2000, through NCBI using the search capabilities of the NIH website, with the nucleotide sequence presented in Figures 9A-9B revealed no significant sequence identity between sequences available in GenBank and nucleic acids 1-4437 of the SEQ ID NO:26.

B4 SUBD2

The paragraph beginning at line 12 on page 25 of the application as filed, has been replaced with paragraph revised as follows:

Two open reading frames were predicted in the rescued sequence using the GENESCAN computer program, which may be found on the Internet using the GENSCAN Web Server of the MIT website, indicating the presence of genes which encode polypeptides of about 124 and 85 amino acids, respectively (Fig. 10A, SEQ ID NO:27 and Fig. 10B, SEQ ID NO:28, respectively).

B5

The paragraph beginning at line 5 on page 14 of the application as filed, has been replaced with paragraph revised as follows:

--In further embodiments, the methods of the invention are carried out using a vector which includes an herbicide resistance gene, conferring resistance to glyphosate-containing herbicides. Glyphosate refers to N-phosphonomethyl glycine, in either its acidic or anionic forms. Herbicides containing this active ingredient include "ROUNDUP" and "GLEAN™". Exemplary genes for imparting glyphosate resistance include an EPSP synthase gene (5-enolpyruvyl-3-phosphosshikimate synthase) (Delanney, *et al.*, 1995; Tinius, *et al.*, 1995), or an acetolactate synthase gene (Yao, *et al.*, 1995).--

B6

The paragraph beginning at page 2, line 1 of the application as filed, has been replaced with paragraph revised as follows:

--Insertional mutagenic techniques have also been used to generate random modifications of native plant genes. For example, the T-DNA insertion technique, termed "T-DNA tagging" or "activation tagging" has been used to develop large numbers of transformed

B7

plant lines, *e.g.*, in *Arabidopsis* (Christensen, S., *et al.*, 9th INTL. CONF. ON ARABIDOPSIS RES. June 24-28, 1998, p 165, Univ. Of Wis.), as well as in the legume, *Medicago truncatula* (Kardailsky, I, *et al.*, 9th INTL. CONF. ON ARABIDOPSIS RES. June 24-28, 1998, p.187-188, Univ. Of Wis.). In this technique, seeds are transformed with the Ti plasmid from *Agrobacterium tumifaciens* which is inserted randomly into the plant genome. See, *e.g.*, Feldmann, KA, *Plant J.* 1:71, 1991; Hayashi H *et al., Science* 258 (5086):1350-3, 1992; Walden, R., *et al.*, Plant Molecular Biology, 26:1521, 1994. The isolation of the floral inducer FLOWERING LOCUS T (FT), which acts in parallel with the meristem-identity gene LEAFY (LFY) to induce flowering in Arabidopsis using activation tagging has recently been described (Kardailsky I *et al.*, Science 286(5446):1962-5, 1999).--

B7 cont

The paragraph beginning at page 7, line 3 of the application as filed, has been replaced with paragraph revised as follows:

--As used herein, the term "sequence identity" means nucleic acid or amino acid sequence identity in two or more aligned sequences, aligned using a sequence alignment program. Sequence searches are preferably carried out using the BLASTN program when evaluating the of a given nucleic acid sequence relative to nucleic acid sequences in the GenBank DNA Sequences and other public databases. The BLASTX program is preferred for searching nucleic acid sequences which have been translated in all reading frames against amino acid sequences in the GenBank Protein Sequences and other public databases. Both BLASTN and BLASTX are run using default parameters of an open gap penalty of 11.0, and an extended gap penalty of 1.0, and utilize the BLOSUM-62 matrix. See, Altschul, *et al.*, Nucl. Acids Res. 25(17) 3389-3402 (1997).--

B8

The paragraph beginning at page 8, line 38 of the application as filed, has been replaced with paragraph revised as follows:

--A fraction of the plants in which the expression of native genes is enhanced will exhibit desired traits. The plants which exhibit such desired traits are selected and the plant genomic DNA flanking the insertion site of the enhancer sequence of the activation tagging nucleic acid construct identified and characterized. Techniques routinely employed by those of skill in the art for identification and isolation of genes of interest are plasmid rescue (Behringer, F.J and Medford, J.I., *Plant Mol. Biol. Reporter* 10: 190-198, 1992), and genome walking (*e.g.*, GenomeWalker™ from Clontech, Palo Alto, CA).--

B9

The paragraph beginning at page 9, line 6 of the application as filed, has been replaced with paragraph revised as follows:

--In some cases, inverse PCR may be used to isolate DNA adjacent known sequence in genomic DNA, by use of oligonucleotide primers complementary to one end of a known

B10